

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Sutcliffe, Gregor J.
de Lecea, Luis
Siggins, George R.
Henriksen, Steven J.
- (ii) TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,
COMPOSITIONS AND METHODS
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
 - (B) STREET: 10666 North Torrey Pines Road, TPC-8
 - (C) CITY: La Jolla
 - (D) STATE: California
 - (E) COUNTRY: US
 - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Schmonsees, William
 - (B) REGISTRATION NUMBER: 31,796
 - (C) REFERENCE/DOCKET NUMBER: 22908-0002
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 30..368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAGCACAGA CTTCAGGTTT CCAAGGAGG ATG GGT GGC TGC AGC ACA AGA GGC
53
Met Gly Gly Cys Ser Thr Arg Gly
1 5

AAG CGG CCG TCA GCC CTC AGT CTG CTG CTG CTG CTG CTG CTC TCG GGC
101
Lys Arg Pro Ser Ala Leu Ser Leu Leu Leu Leu Leu Leu Ser Gly
10 15 20

ATC GCA GCC TCT GCC CTC CCC CTG GAG AGC GGT CCC ACC GGC CAG GAC
149
Ile Ala Ala Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp
25 30 35 40

AGT GTG CAG GAT GCC ACA GGC GGG AGG AGG ACC GGC CTT CTG ACT TTC
197
Ser Val Gln Asp Ala Thr Gly Gly Arg Arg Thr Gly Leu Leu Thr Phe
45 50 55

CTT GCC TGG TGG CAT GAG TGG GCT TCC CAA GAC AGC TCC AGC ACC GCT
245
Leu Ala Trp Trp His Glu Trp Ala Ser Gln Asp Ser Ser Ser Thr Ala
60 65 70

TTC GAA GGG GGT ACC CCG GAG CTG TCT AAG CGG CAG GAA AGA CCA CCC
293
Phe Glu Gly Gly Thr Pro Glu Leu Ser Lys Arg Gln Glu Arg Pro Pro
75 80 85

CTC CAG CAG CCC CCA CAC CGG GAT AAA AAG CCC TGC AAG AAC TTC TTC
341
Leu Gln Gln Pro Pro His Arg Asp Lys Lys Pro Cys Lys Asn Phe Phe
90 95 100

TGG AAA ACC TTC TCC TCG TGC AAG TAGCCCGAGC CTGACCGGAG CCTGACCGGC
395
Trp Lys Thr Phe Ser Ser Cys Lys
105 110

CACCCTGTGA ATGCAGCCGT GGCCTGAATA AAGAGTGTCA AGT
438

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Gly	Cys	Ser	Thr	Arg	Gly	Lys	Arg	Pro	Ser	Ala	Leu	Ser	Leu
1				5				10						15	
Leu	Leu	Leu	Leu	Leu	Leu	Ser	Gly	Ile	Ala	Ala	Ser	Ala	Leu	Pro	Leu
			20					25					30		
Glu	Ser	Gly	Pro	Thr	Gly	Gln	Asp	Ser	Val	Gln	Asp	Ala	Thr	Gly	Gly
		35				40						45			
Arg	Arg	Thr	Gly	Leu	Leu	Thr	Phe	Leu	Ala	Trp	Trp	His	Glu	Trp	Ala
	50					55					60				
Ser	Gln	Asp	Ser	Ser	Ser	Thr	Ala	Phe	Glu	Gly	Gly	Thr	Pro	Glu	Leu
65					70					75					80
Ser	Lys	Arg	Gln	Glu	Arg	Pro	Pro	Leu	Gln	Gln	Pro	Pro	His	Arg	Asp
			85					90						95	
Lys	Lys	Pro	Cys	Lys	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Ser	Ser	Cys	Lys
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln	Cys	Ala	Leu	Ala	Ala	Leu	Cys	Ile	Val	Leu	Ala	Leu	Gly	Gly	Val
1				5				10					15		

Thr	Gly	Ala	Pro	Ser	Asp	Pro	Arg	Leu	Arg	Gln	Phe	Leu	Gln	Lys	Ser
			20					25					30		
Leu	Ala	Ala	Ala	Thr	Gly	Lys	Gln	Glu	Leu	Ala	Lys	Tyr	Phe	Leu	Ala
	35					40					45				
Glu	Leu	Leu	Ser	Glu	Pro	Asn	Gln	Thr	Glu	Asn	Asp	Ala	Leu	Glu	Pro
	50					55					60				
Glu	Asp	Leu	Pro	Gln	Ala	Ala	Glu	Gln	Asp	Glu	Met	Arg	Leu	Glu	Leu
65					70					75					80
Gln	Arg	Ser	Ala	Asn	Ser	Asn	Pro	Ala	Met	Ala	Pro	Arg	Glu	Arg	Lys
				85					90					95	
Ala	Gly	Cys	Lys	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Thr	Ser	Cys		
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 25..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCACGAGGCT CAGCACGTCC GAGG ATG ATG GGT GGC CGA GGC ACA GGA GGC
51

Met Met Gly Gly Arg Gly Thr Gly Gly
1 5

AAG TGG CCC TCA GCC TTC GGG CTG CTG CTG CTC TGG GGG GTC GCA GCC
99

Lys Trp Pro Ser Ala Phe Gly Leu Leu Leu Leu Trp Gly Val Ala Ala
10 15 20 25

TCC GCC CTT CCC CTG GAG AGT GGC CCT ACT GGC CAG GAC AGT GTG CAG
147

Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
30 35 40

GAA GCC ACC GAG GGG AGG AGC GGC CTT CTG ACT TTC CTT GCC TGG TGG
195
Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp
45 50 55

CAC GAG TGG GCT TCC CAA GCC AGC TCC AGC ACC CCC GTC GGA GGG GGT
243
His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly
60 65 70

ACC CCC GGG CTG TCC AAG AGC CAG GAA AGG CCA CCC CCC CAA CAG CCC
291
Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Pro Gln Gln Pro
75 80 85

CCA CAC CTG GAT AAA AAG CCC TGC AAG AAC TTC TTC TGG AAA ACC TTC
339
Pro His Leu Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe
90 95 100 105
TCC TCG TGC AAG TAACCCACCC CTGGGCATAG CACCCTGGCC ACCCTGTGAG
391
Ser Ser Cys Lys
110

ATGCCAACGA GACCTGAATA AAGACTGTCA ATCAAC
427

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Met Gly Gly Arg Gly Thr Gly Gly Lys Trp Pro Ser Ala Phe Gly
1 5 10 15
Leu Leu Leu Leu Trp Gly Val Ala Ala Ser Ala Leu Pro Leu Glu Ser
20 25 30
Gly Pro Thr Gly Gln Asp Ser Val Gln Glu Ala Thr Glu Gly Arg Ser
35 40 45
Gly Leu Leu Thr Phe Leu Ala Trp Trp His Glu Trp Ala Ser Gln Ala
50 55 60
Ser Ser Ser Thr Pro Val Gly Gly Gly Thr Pro Gly Leu Ser Lys Ser
65 70 75 80

Gln Glu Arg Pro Pro Pro Gln Gln Pro Pro His Leu Asp Lys Lys Pro
85 90 95

Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
100 105

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser	Ala	Leu	Pro	Leu	Glu	Ser	Gly	Pro	Thr	Gly	Gln	Asp	Ser	Val	Gln
1				5					10					15	
Asp	Ala	Thr	Gly	Gly	Arg	Arg	Thr	Gly	Leu	Leu	Thr	Phe	Leu	Ala	Trp
			20					25					30		
Trp	His	Glu	Trp	Ala	Ser	Gln	Asp	Ser	Ser	Ser	Thr	Ala	Phe	Glu	Gly
		35					40					45			
Gly	Thr	Pro	Glu	Leu	Ser	Lys	Arg	Gln	Glu	Arg	Pro	Pro	Leu	Gln	Gln
	50					55					60				
Pro	Pro	His	Arg	Asp	Lys	Lys	Pro	Cys	Lys	Asn	Phe	Phe	Trp	Lys	Thr
65					70					75					80
Phe	Ser	Ser	Cys	Lys											
				85											

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp Lys Lys Pro
1 5 10 15

Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
20 25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
1 5 10 15
Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp
20 25 30
His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly
35 40 45
Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Pro Gln Gln Pro
50 55 60
Pro His Leu Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe
65 70 75 80
Ser Ser Cys Lys

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Glu Arg Pro Pro Pro Gln Gln Pro Pro His Leu Asp Lys Lys Pro
1 5 10 15
Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
20 25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gln Glu Arg Pro Pro Pro Gln Gln Pro Pro His Leu Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCGAGATCT AAGGAGGATG GGTGGCTGCA G
31

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTGTCTAGA TCATAGGTCT TCTTCTGATA TTAGTTTTTG TTCCTTGCAC GAGGAGAAGG
60

TTTTCCAG
68

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATCGAGATCT GCCCTCCCCC TGGAGA
26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACTGAATTCA GGCCACGGCT GCATTCACAG
30

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Lys Arg Pro Ser Ala
1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Lys Trp Pro Ser Ala
1 5

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp Trp His Glu Trp Ala
1 5

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCAAGCGGC CGTCAGCC
18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGCAAGTGGC CCTCAGCC
18

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCCCACTCA TGCCACCA
18

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr	Pro	Cys	Lys	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Ser	Ser	Cys	Lys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro	Cys	Lys	Asn	Phe	Phe	Tyr	Lys	Thr	Phe	Ser	Ser	Cys	Lys
1				5					10				

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 701 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CC AAAACATTGA TTTCAGGGCT GCCAGGAAGG AAGAGCAGCA GCAGGGTGGG
52

AGAGAAGCTC CAGTCAGCCC ACAAGATGCC ATTGTCCCCC GGCCTCCTGC TGCTGCTGCT
112

CTCCGGGGCC ACGGCCACCG CTGCCCTGCC CCTGGAGGGT GGCCCCACCG GCCGAGACAG
172

CGAGCATATG CAGGAAGCGG CAGGAATAAG GAAAAGCAGC CTCCTGACTT TCCTCGCTTG
232

GTGGTTTGAG TGGACCTCCC AGGCCAGTGC CGGGCCCCTC ATAGGAGAGG AAGCCCGGGA
292

GGTGGCCAGG CGGCAGGAAG GCGCACCCCC CCAGCAATCC GCGCGCCGGG ACAGAATGCC
352

CTGCAGGAAC TTCTTCTGGA AGACCTTCTC CTCCTGCAA TAAACCTCA CCCATGAATG
412

CTCACGCAAG TGTAATGACA GACCTGAATA AAATGTATTA AGCAGCAGTG ATCTTTCCTC
472

TCCTCCTTCC CAAGTCATTG AAAAGTGTTT GTTATTTAAA TTCCAATAAT GCCCAATACT
532

GACGTGTCTT GAGTAATTTG GAACCCAAAA GTGAAGATCT TTGATAAAGA TTTTTTTTGT
592

GGTTCGACTG GACTGTGCTG AGTGCGGGCA CTGGGCTTTT CTTCTGATGT TCATTATGGT
652

GCTGGGAAGC TCTGTCTTTG ATTTAAAATA AAATAGCTAA AGGCTACAC
701

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Pro	Leu	Ser	Pro	Gly	Leu	Leu	Leu	Leu	Leu	Ser	Gly	Ala	Thr
1				5				10					15	

Ala	Thr	Ala	Ala	Leu	Pro	Leu	Glu	Gly	Gly	Pro	Thr	Gly	Arg	Asp	Ser
			20					25					30		
Glu	His	Met	Gln	Glu	Ala	Ala	Gly	Ile	Arg	Lys	Ser	Ser	Leu	Leu	Thr
		35					40					45			
Phe	Leu	Ala	Trp	Trp	Phe	Glu	Trp	Thr	Ser	Gln	Ala	Ser	Ala	Gly	Pro
	50					55					60				
Leu	Ile	Gly	Glu	Glu	Ala	Arg	Glu	Val	Ala	Arg	Arg	Gln	Glu	Gly	Ala
65					70					75					80
Pro	Pro	Gln	Gln	Ser	Ala	Arg	Arg	Asp	Arg	Met	Pro	Cys	Arg	Asn	Phe
				85					90					95	
Phe	Trp	Lys	Thr	Phe	Ser	Ser	Cys	Lys							
			100					105							

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